RAW SEQUENCE LISTING

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Application Serial Number: _10/801,292_

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PATENT APPLICATION: **US/10/801,292**   TIME: 11:11:32

Input Set : **A:\5422-2.app**
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 3 <110> APPLICANT: LEE, YI-CHAO
 4        YUEN, PUI-YEE
 5        HUANG, YI-HUEI
 6        WU, HUI-CHUAN
 8 <120> TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 9        THERAPY OF CANCER
11 <130> FILE REFERENCE: 5422-2
13 <140> CURRENT APPLICATION NUMBER: 10/801,292
14 <141> CURRENT FILING DATE: 2004-03-15
16 <160> NUMBER OF SEQ ID NOS: 21
18 <170> SOFTWARE: PatentIn Ver. 3.2
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21 <211> LENGTH: 2096
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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28 cccttagtcg cgccccggcc ctcccgctgc ccggagtccg gcggccacga ggcccagccg 180
29 cgtcctcccg cgcttgctcg cccggcggcc gcagccatgt cccggggggcc cgaggaggtg 240
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32 aaagcctact acgatggagt ggccaagatc ggtgagattg ccactgggtc ccccgtgtca 420
33 actgaactgg gacatgtcct catagagatt tcaagtaccc acaagaaact caacgagagt 480
34 cttgatgaaa attttaaaaa attccacaaa gagattatcc atgagctgga gaagaagata 540
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37 ggaagccgaa acgcactcaa atatgaacac aaagaaattg agtatgtgga gaccgttact 720
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39 gagaagaggc gcttctgctt tctggttgat aagcactgtg gctttgcaaa ccacatacat 840
40 tattatcact tacagtctgc agaactactg aattccaagc tgcctcggtg gcaggagacc 900
41 tgtgttgatg ccatcaaagt gccagagaaa atcatgaata tgatcgaaga aataaagacc 960
42 ccagcctcta cccccgtgtc tggaactcct caggcttcac ccatgatcga gagaagcaat 1020
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56 atgatgggcg catcctgtct gccacgtgct gacggtcggg aagcttcagt ggagaggcct 1860
57 aactctaatg tcgcctgctt aagcaaatca tgcttctctg tttcacgtag ttgggttgac 1920
58 aagtttctgc ctttaagata aatgagtaat agtctaatga ccagctcagc catttaaaat 1980
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73   20   25   30
75 Leu Gly Lys Asn Tyr Glu Lys Ala Val Asn Ala Met Ile Leu Ala Gly
76   35   40   45
78 Lys Ala Tyr Tyr Asp Gly Val Ala Lys Ile Gly Glu Ile Ala Thr Gly
79   50   55   60
81 Ser Pro Val Ser Thr Glu Leu Gly His Val Leu Ile Glu Ile Ser Ser
82 65   70   75   80
84 Thr His Lys Lys Leu Asn Glu Ser Leu Asp Glu Asn Phe Lys Lys Phe
85   85   . 90   95
87 His Lys Glu Ile Ile His Glu Leu Glu Lys Lys Ile Glu Leu Asp Val
88   100   105   110
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91   115   120   125
93 Lys Leu Glu Ser Leu Glu Lys Ser Gln Ala Glu Leu Lys Lys Ile Arg
94   130   135   140
96 Arg Lys Ser Gln Gly Ser Arg Asn Ala Leu Lys Tyr Glu His Lys Glu
97 145   150   155   160
99 Ile Glu Tyr Val Glu Thr Val Thr Ser Arg Gln Ser Glu Ile Gln Lys
100   165   170   175
102 Phe Ile Ala Asp Gly Cys Lys Glu Ala Leu Leu Glu Glu Lys Arg Arg
103   180   185   190
105 Phe Cys Phe Leu Val Asp Lys His Cys Gly Phe Ala Asn His Ile His
106   195   200   205
108 Tyr Tyr His Leu Gln Ser Ala Glu Leu Leu Asn Ser Lys Leu Pro Arg
109   210   215   220
111 Trp Gln Glu Thr Cys Val Asp Ala Ile Lys Val Pro Glu Lys Ile Met
112 225   230   235   240
114 Asn Met Ile Glu Glu Ile Lys Thr Pro Ala Ser Thr Pro Val Ser Gly
115   245   250   255
117 Thr Pro Gln Ala Ser Pro Met Ile Glu Arg Ser Asn Val Val Arg Lys
118   260   265   270
120 Asp Tyr Asp Thr Leu Ser Lys Cys Ser Pro Lys Met Pro Pro Ala Pro
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129 Ser Glu Asp Pro Ser Leu Gln Arg Ser Val Ser Val Ala Thr Gly Leu
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132 Asn Met Met Lys Lys Gln Lys Val Lys Thr Ile Phe Pro His Thr Ala
133         340             345             350
135 Gly Ser Asn Lys Thr Leu Leu Ser Phe Ala Gln Gly Asp Val Ile Thr
136         355             360             365
138 Leu Leu Ile Pro Glu Glu Lys Asp Gly Trp Leu Tyr Gly Glu His Asp
139     370             375             380
141 Val Ser Lys Ala Arg Gly Trp Phe Pro Ser Ser Tyr Thr Lys Leu Leu
142 385             390             395             400
144 Glu Glu Asn Glu Thr Glu Ala Val Thr Val Pro Thr Pro Ser Pro Thr
.145            405             410             415
147 Pro Val Arg Ser Ile Ser Thr Val Asn Leu Ser Glu Asn Ser Ser Val
148             420             425             430
150 Val Ile Pro Pro Pro Asp Tyr Leu Glu Cys Leu Ser Met Gly Ala Ala
151         435             440             445
153 Ala Asp Arg Arg Ala Asp Ser Ala Arg Thr Thr Ser Thr Phe Lys Ala
154     450             455             460
156 Pro Ala Ser Lys Pro Glu Thr Ala Ala Pro Asn Asp Ala Asn Gly Thr
157 465             470             475             480
159 Ala Lys Pro Pro Phe Leu Ser Gly Glu Asn Pro Phe Ala Thr Val Lys
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174 atggtctaga ggctggagat tcaagatctg ggtgccatca tttctctggtt ctgttgatga 180
175 ccctcttcca ggttacatac agcttacatc ttgcatcctc aagcgttttt cttataaggc 240
176 taaaaattca caaagcatat atcaatgaat caggaggatc tagatccgga tagtactaca 300
177 gatgtgggag atgttacaaa tactgaagaa gaacttatta gagaatgtga agaaatgtgg 360
178 aaagatatgg aagaatgtca gaataaatta tcacttattg gaactgaaac actcaccgat 420
179 tcaaatgctc agctatcatt gttaattatg caagtaaaat gtttaaccgc tgaactcagt 480
180 caatggcaga aaaaaacacc tgaaacaatt cccttgactg aagacgttct cataacatta 540
181 ggaaaagaag agttccaaaa gctgagacaa gatcttgaaa tggtactgtc cactaaggag 600
182 tcaaagaatg aaaagttaaa ggaagactta gaaagggaac aacggtggtt ggatgaacag 660
183 caacagataa tggaatctct taatgtacta cacagtgaat tgaaaaataa ggttgaaaca 720
184 ttttctgaat caagaatctt taatgaactg aaaactaaaa tgcttaatat aaaagaatat 780
185 aaggagaaac tcttgagtac cttgggcgag tttctagaag accatttttcc tctgcctgat 840
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217   35   40   45
219 Thr Leu Thr Asp Ser Asn Ala Gln Leu Ser Leu Leu Ile Met Gln Val
220   50   55   60
222 Lys Cys Leu Thr Ala Glu Leu Ser Gln Trp Gln Lys Lys Thr Pro Glu
223 65   70   75   80
225 Thr Ile Pro Leu Thr Glu Asp Val Leu Ile Thr Leu Gly Lys Glu Glu
226   85   90   95
228 Phe Gln Lys Leu Arg Gln Asp Leu Glu Met Val Leu Ser Thr Lys Glu
229   100   105   110
231 Ser Lys Asn Glu Lys Leu Lys Glu Asp Leu Glu Arg Glu Gln Arg Trp
232   115   120   125
234 Leu Asp Glu Gln Gln Gln Ile Met Glu Ser Leu Asn Val Leu His Ser
235   130   135   140
237 Glu Leu Lys Asn Lys Val Glu Thr Phe Ser Glu Ser Arg Ile Phe Asn
238 145   150   155   160
240 Glu Leu Lys Thr Lys Met Leu Asn Ile Lys Glu Tyr Lys Glu Lys Leu
241   165   170   175
243 Leu Ser Thr Leu Gly Glu Phe Leu Glu Asp His Phe Pro Leu Pro Asp
244   180   185   190
246 Arg Ser Val Lys Lys Lys Lys Asn Ile Gln Glu Ser Ser Val Asn
247   195   200   205
249 Leu Ile Thr Leu His Glu Met Leu Glu Ile Leu Ile Asn Arg Leu Phe
250   210   215   220
252 Asp Val Pro His Asp Pro Tyr Val Lys Ile Ser Asp Ser Phe Trp Pro
253 225   230   235   240

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263 <211> LENGTH: 1660
264 <212> TYPE: DNA
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310 Glu Glu Met Leu Gly Lys Lys Gln Glu Tyr Leu Glu Asn Arg Ile Gln
311             35                  40                  45
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